

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/560,303
Source: FWP
Date Processed by STIC: 12/20/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

10/560,303

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
 Wrapped Aminos was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will
 prevent "wrapping."

- 2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

- 3 Misaligned Amino The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers;
 Numbering use **space characters**, instead.

- 4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. Please
 ensure your subsequent submission is saved in **ASCII** text.

- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules,**
 each n or Xaa can only represent a single residue. Please present the **maximum** number of each
 residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 PatentIn 2.0 A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
 "bug" sequences(s) . Normally, PatentIn would automatically generate this section from the
 previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
 the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for**
 Artificial or Unknown sequences.

- 7 Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (OLD RULES) (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

- 8 Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 (NEW RULES) <210> sequence id number
 <400> sequence id number
 000

- 9 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
 (NEW RULES) Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

- 10 Invalid <213> Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
 Response scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or
 is Artificial Sequence

- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or
 "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

- 12 PatentIn 2.0 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
 "bug" resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
 listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWP

RAW SEQUENCE LISTING

DATE: 12/20/2005

PATENT APPLICATION: US/10/560,303

TIME: 11:21:39

Input Set : A:\601-1-131 PCT US NATL PHASE SEQUENCE LISTING.txt

Output Set: N:\CRF4\12202005\J560303.raw

4 <110> APPLICANT: Inouye, Masayori
 5 Zhang, Junjie
 6 Zhang, Yong Long
 7 Qing, Guoliang
 8 Suzuki, Motoo
 10 <120> TITLE OF INVENTION: mRNA Interferases and Methods of Use Thereof
 12 <130> FILE REFERENCE: University of Medicine & Dentistry of New Jersey (601-1-131PCT)
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/560,303
 C--> 15 <141> CURRENT FILING DATE: 2005-12-12
 17 <150> PRIOR APPLICATION NUMBER: 60/543,693
 18 <151> PRIOR FILING DATE: 2004-02-11
 20 <150> PRIOR APPLICATION NUMBER: 60/478,515
 21 <151> PRIOR FILING DATE: 2003-06-13
 23 <160> NUMBER OF SEQ ID NOS: 92
 25 <170> SOFTWARE: FastSEQ for Windows Version 4.0

pp 1-4

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

1411 <210> SEQ ID NO: 89
 1412 <211> LENGTH: 17
 1413 <212> TYPE: RNA
 1414 <213> ORGANISM: Artificial Sequence
 1416 <220> FEATURE:
 1417 <223> OTHER INFORMATION: mRNA transcript
 1419 <400> SEQUENCE: 89
 E--> 1420 aatgatgaca ctggaag
 1422 <210> SEQ ID NO: 90
 1423 <211> LENGTH: 17
 1424 <212> TYPE: RNA
 1425 <213> ORGANISM: Artificial Sequence
 1427 <220> FEATURE:
 1428 <223> OTHER INFORMATION: mRNA transcript
 1430 <400> SEQUENCE: 90
 E--> 1431 gtcggtgaca ttgatgg
 1433 <210> SEQ ID NO: 91
 1434 <211> LENGTH: 17
 1435 <212> TYPE: RNA
 1436 <213> ORGANISM: Artificial Sequence
 1438 <220> FEATURE:
 1439 <223> OTHER INFORMATION: mRNA transcript
 1441 <400> SEQUENCE: 91
 E--> 1442 atctgaaca cgcagcc

insufficient explanation - give source
 of genetic material
 (see item 11 on
 Error Summary
 sheet)
 no t's allowed in an RNA sequence
 (for a combined
 DNA/RNA sequence,
 use <212> DNA
 and explain in
 <220>-<223>
 section)
 same error

17
 17
 this error appears throughout Sequence Listing

RAW SEQUENCE LISTING

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Input Set : A:\601-1-131 PCT US NATL PHASE SEQUENCE LISTING.txt

Output Set: N:\CRF4\12202005\J560303.raw

1444 <210> SEQ ID NO: 92

1445 <211> LENGTH: 17

1446 <212> TYPE: RNA

1447 <213> ORGANISM: Artificial Sequence

1449 <220> FEATURE:

1450 <223> OTHER INFORMATION: mRNA transcript

1452 <400> SEQUENCE: 92

E--> 1453 ~~tcgtttt~~aca ccgttga

17

see p. 3 for more error

10/560,303 3

<210> 14

<211> 23

<212> DNA

<213> Artificial Sequence

need explanation
(see p. 4)

<400> 14

agatctcgat cccgcaaatt aat

23

same error in sequence 30

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/560,303

DATE: 12/20/2005
TIME: 11:21:40

Input Set : A:\601-1-131 PCT US NATL PHASE SEQUENCE LISTING.txt
Output Set: N:\CRF4\12202005\J560303.raw

Use of <220> Feature(NEW RULES):

Sequence(s) are missing the <220> Feature and associated headings.

Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32) (Sec.1.823 of new Rules)

Seq#:14,30

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/560,303

DATE: 12/20/2005

TIME: 11:21:40

Input Set : A:\601-1-131 PCT US NATL PHASE SEQUENCE LISTING.txt

Output Set: N:\CRF4\12202005\J560303.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application Number
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:240 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:14, <213>
ORGANISM:Artificial Sequence
L:240 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:14, <213>
ORGANISM:Artificial Sequence
L:240 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:14,Line#:240
L:414 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:30, <213>
ORGANISM:Artificial Sequence
L:414 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:30, <213>
ORGANISM:Artificial Sequence
L:414 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:30,Line#:414
L:1420 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:3
L:1431 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:6
L:1442 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:2
L:1453 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:7